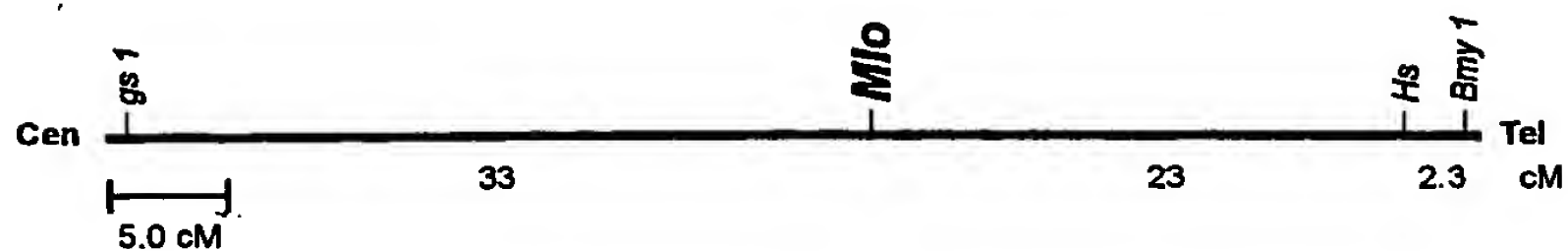




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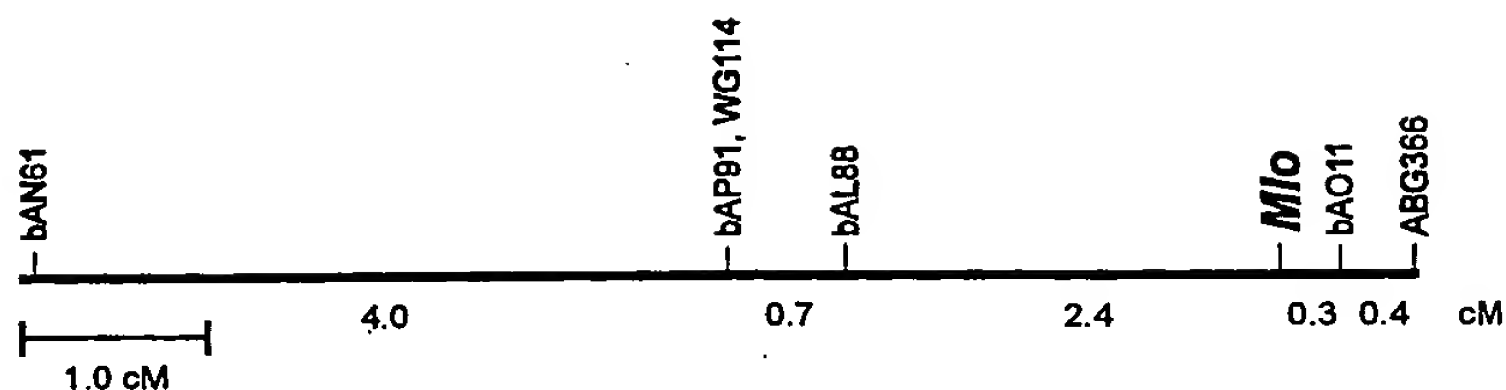
Figure 1

Morphological
marker map



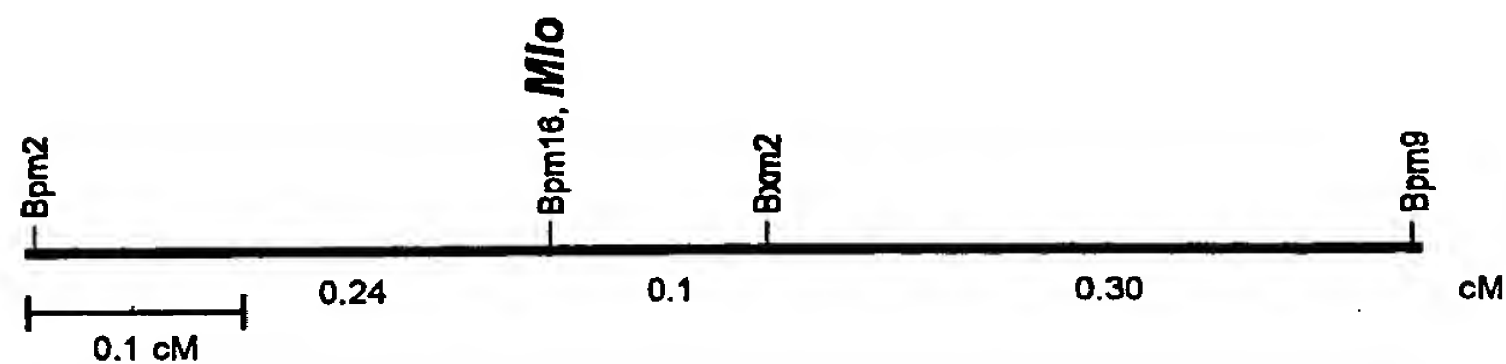
RFLP map

(Carlsberg II *Mlo* x
Grannenlose Zweizeilige *mlo-11*)

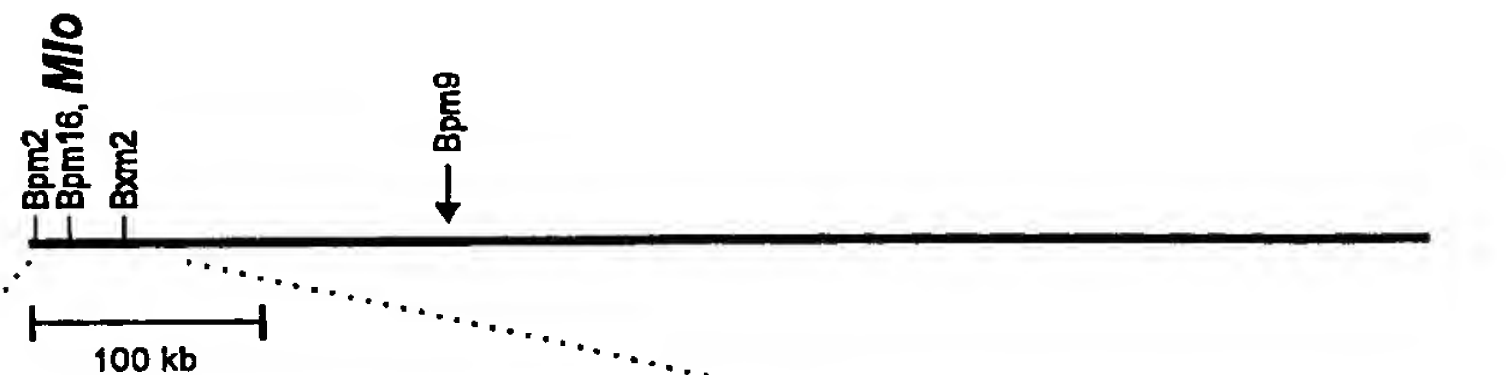


AFLP map

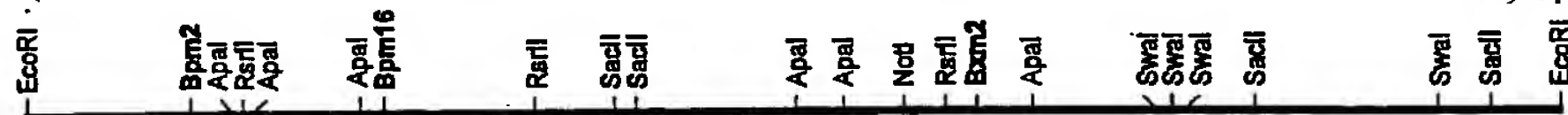
(Ingrid *Mlo* x BC Ingrid *mlo-3*)



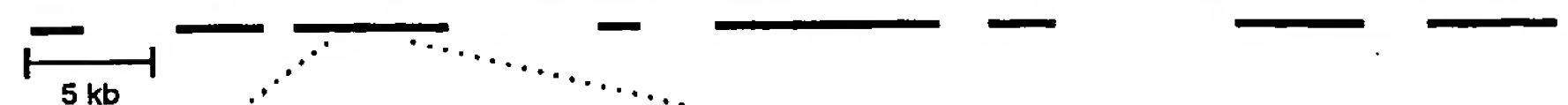
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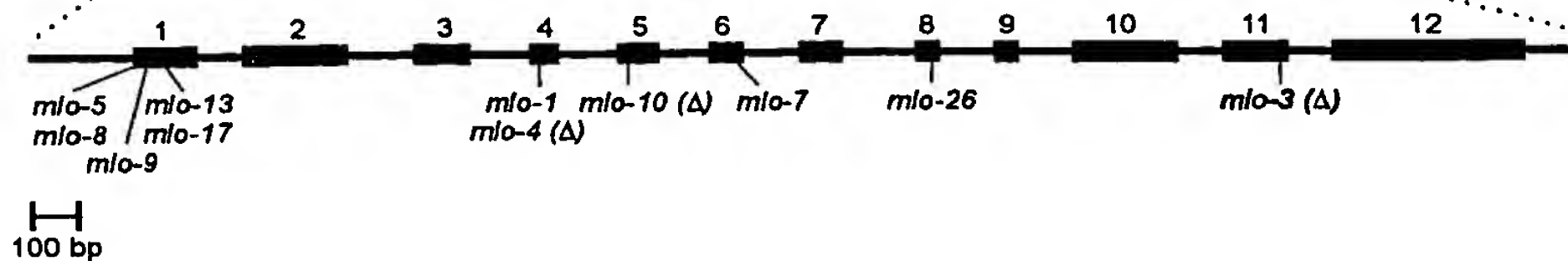
BAC F15



Sequence contigs



Mlo gene structure





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Figure 2A

M S D K K G V P A R E L P E T P S W A V ATGTCGGACAAAAAGGGGTGCCGGCGCGGGAGCTGCCGGAGACGCCGTCGTGGGCGGTG	60
A V V F A A M V L V S V L M E H G L H K GCGGTGGTCTTCGCCGCCATGGTGCTCGTGTCCGTCCTCATGGAACACGGCCTCCACAAG	120
L G H W F Q H R H K K A L W E A L E K M CTCGGCCATTGGTTCCAGCACCGGCACAAGAAGGCCCTGTGGGAGGCGCTGGAGAAGATG	180
K A E L M L V G F I S L L L I V T Q D P AAGGCGGAGCTCATGCTGGTGGGCTTCATATCCCTGCTCCTCATCGTCACGCAGGACCCC	240
I I A K I C I S E D A A D V M W P C K R ATCATCGCCAAGATATGCATCTCCGAGGATGCCGCCGACGTCATGTGGCCCTGCAAGCGC	300
G T E G R K P S K Y V D Y C P E G K V A GGCACCAGGGCCGCAAGCCCAGCAAGTACGTTGACTACTGCCCGGAGGGCAAGGTGGCG	360
L M S T G S L H Q L H V F I F V L A V F CTCATGTCCACGGGCAGCTTGCACCAGCTGCACGTCTTCATCTTCGTGCTCGCGGTCTTC	420
H V T Y S V I T I A L S R L K M R T W K CATGTCACCTACAGCGTCATCACCATAGCTCTAAGCCGTCTCAAATGAGAACATGGAAG	480
K W E T E T T S L E Y Q F A N D P A R F AAATGGGAGACAGAGACCACCTCCTTGAATACCAGTTCGCAAATGATCCTGCACGGTTC	540
R F T H Q T S F V K R H L G L S S T P G CGGTTACGCACCAGACGTCGTTCGTGAAGCGCCACCTGGGCCTCTCCAGCACCCCTGGC	600
I R W V V A F F R Q F F R S V T K V D Y ATCAGATGGGTGGTGGCCTTCTTCAGGCAGTTCTTCAGGTCAGTCACCAAGGTGGACTAC	660
L T L R A G F I N A H L S Q N S K F D F CTGACCTTGAGGGCAGGCTTCATCAACGCGCATTGTGTCGAAAACAGCAAGTTCGACTTC	720
H K Y I K R S M E D D F K V V V G I S L CACAAGTACATCAAGAGGTGCGATGGAGGACGACTTCAAGGTCGTGCGTCGGCATCAGCCTC	780
P L W G V A I L T L F L D I N G V G T L CCGCTGTGGGGTGTGGCGATCCTCACCTCTTCCTTGACATCAATGGGGTTGGCACGCTC	840
I W I S F I P L V I L L C V G T K L E M ATCTGGATTTCTTTCATCCCTCTCGTGATCCTCTTGTGTGTTGGAACCAAGCTGGAGATG	900
I I M E M A L E I Q D R A S V I K G A P ATCATCATGGAGATGGCCCTGGAGATCCAGGACCGGGCGAGCGTCATCAAGGGGGCCCCC	960
V V E P S N K F F W F H R P D W V L F F GTGGTCGAGCCCAGCAACAAGTTCTTCTGGTTCCACCGCCCCGACTGGGTCCTCTTCTTC	1020
I H L T L F Q N A F Q M A H F V W T V A ATACACCTGACGTTGTTCCAGAACGCGTTTCAGATGGCGCATTTTGTGTGGACAGTGGCC	1080
T P G L K K C Y H T Q I G L S I M K V V ACGCCCCGGCTTGAAGAAATGCTACCACACGCAGATCGGGCTGAGCATCATGAAGGTGGTG	1140
V G L A L Q F L C S Y M T F P L Y A L V GTGGGGCTAGCTCTCCAGTTCCTCTGCAGCTATATGACCTTCCCCCTCTACGCGCTCGTC	1200
T Q M G S N M K R S I F D E Q T S K A L ACACAGATGGGATCAAACATGAAGAGGTCCATCTTCGACGAGCAGACGTCCAAGGCGCTC	1260



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Figure 2B

T N W R N T A K E K K K V R D T D M L M ACCAACTGGCGGAACACGGCCAAGGAGAAGAAGAAAGTCCGAGACACGGACATGCTGATG	1320
A Q M I G D A T P S R G S S P M P S R G GCTCAGATGATCGGCGACGCAACACCGAGCCGAGGCTCGTCGCCGATGCCGAGCCGGGGC	1380
S S P V H L L H K G M G R S D D P Q S A TCATCACCCGTGCACCTGCTTCACAAGGGCATGGGGCGGTTCGGACGACCCCCAGAGCGCG	1440
P T S P R T Q Q E A R D M Y P V V V A H CCCACCTCGCCAAGGACCCAGCAGGAGGCTAGGGACATGTACCCGGTTGTGGTGGCGCAC	1500
P V H R L N P N D R R R S A S S S A L E CCGGTGCACAGACTAAATCCTAACGACAGGAGGAGGTCCGCCTCGTCGTCGGCCCTCGAA	1560
A D I P S A D F S F S Q G * GCCGACATCCCCAGTGCAGATTTTTCCTTCAGCCAGGGATGA	1602



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Figure 3

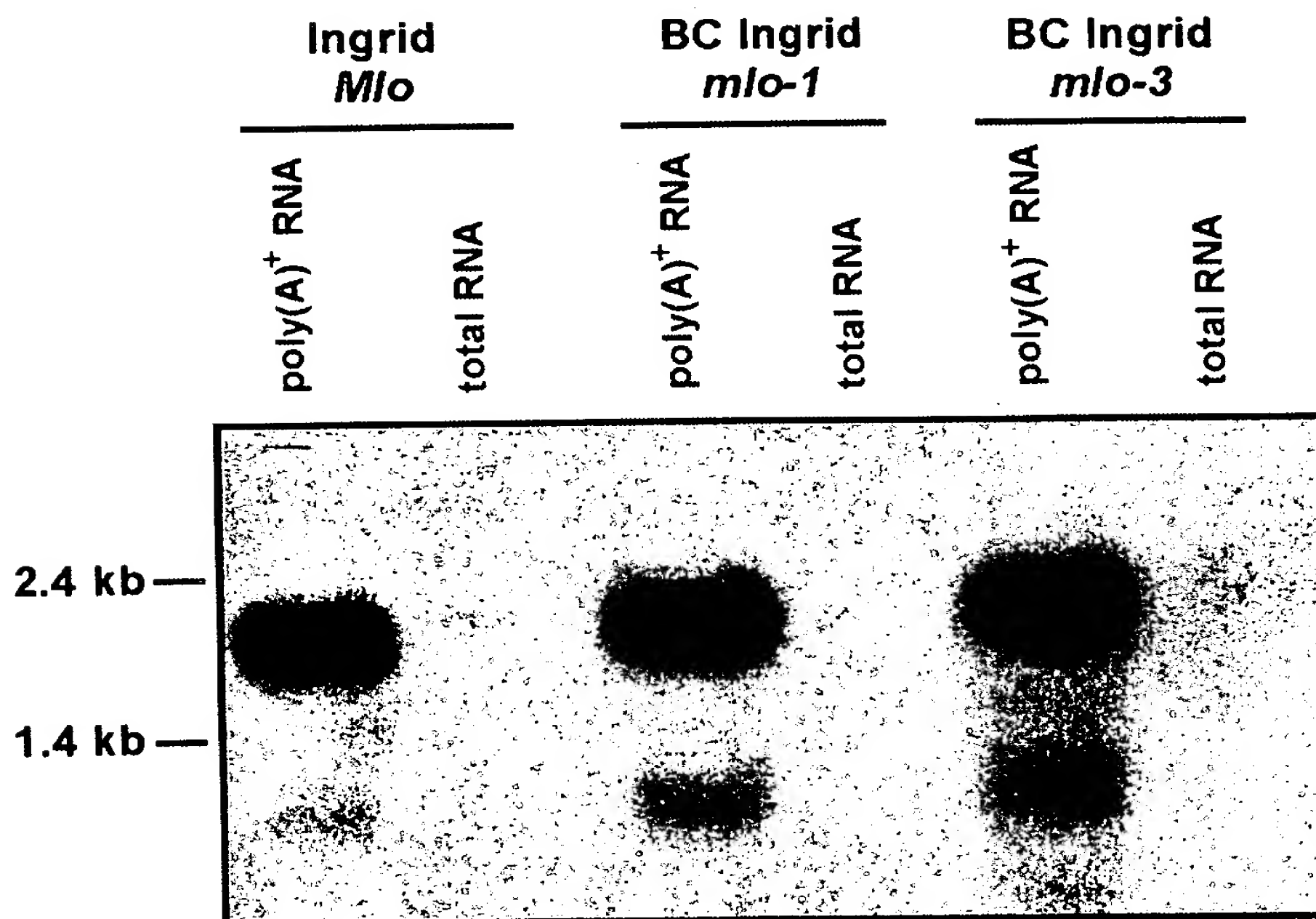


Figure 4B

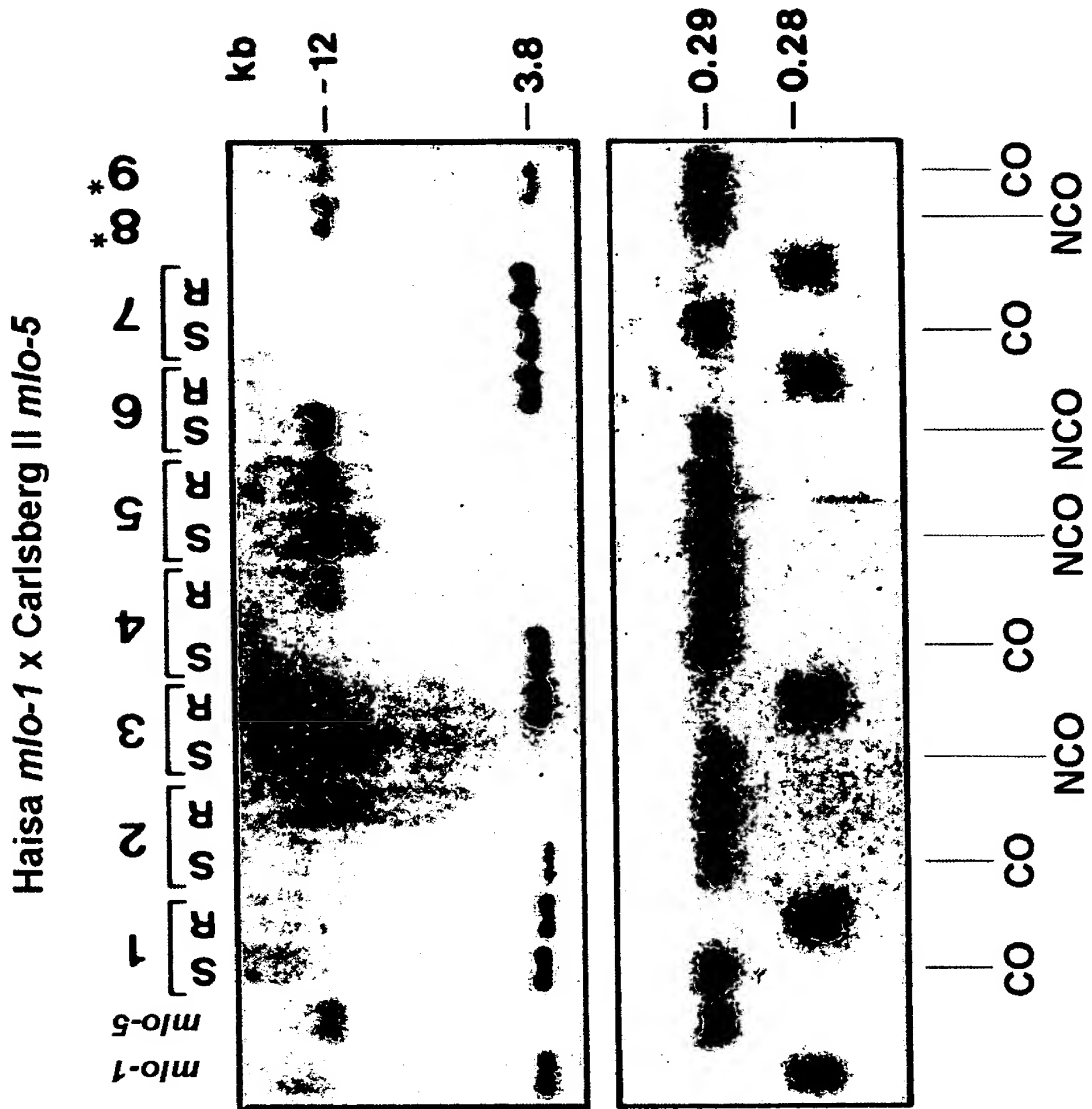
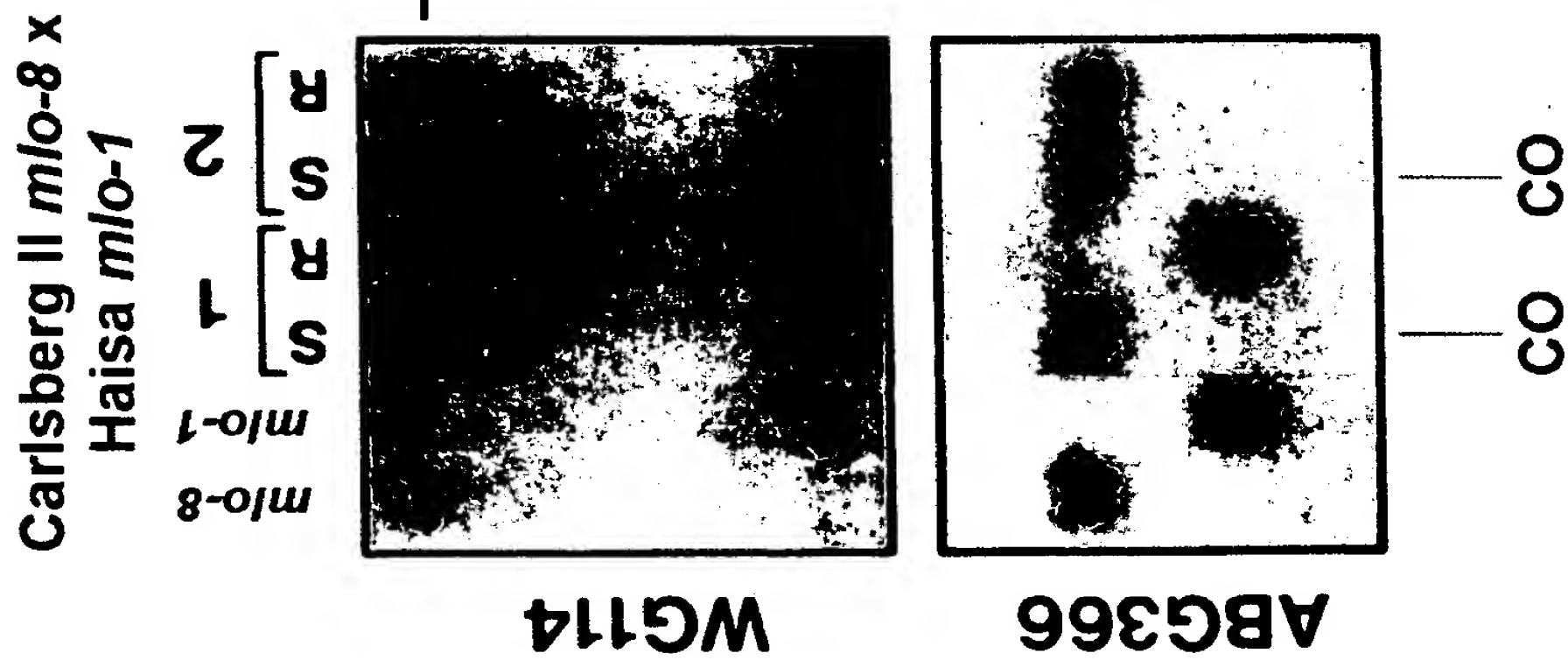


Figure 4A



WG114

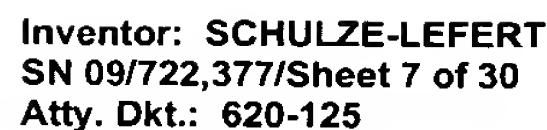
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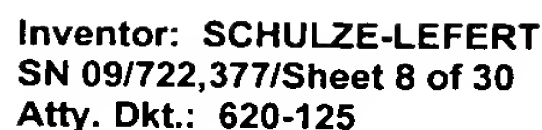
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Figure 5A

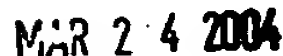
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80 GCANAGCTGATGCTGCTGGGCTTCATNTCCCTGCTTCTCACC GTGGCACA 129
342 GGACCCCATCATCGCCAAGATATGCATCTCCGAGGATGCCGCCGACGTC 391
|| || |||| ||||| : || ||||| || || || || || ||
130 GGCGCC...CATCTCCAANATCTGCATCCCCAAGTCGGCTGCCAACATCT 176
392 TGTGGCCCTGCAAGCGCGGCACCGAGGGCCGC.AAGCCCAGCAAGTACGT 440
||| ||| ||||| ||| : || | | | ||| : | || | ||
177 TGTGCGCGTGCAAGGCAGGCCNAGATGCCATCGAAGAANAAGCAGCAAGT 226
441 TGACTACTGCCCGGAGGTGAGCAGCAGAGCCCGGACCAGCAGCTTCACGA 490
| | : | : | || || || | | | | | | | | | : |
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491 TGATGAAGAAATCAATACC.....GAACTTTTCTTGTTTCT 528
| | | | | : || | | | | : : :
276 TCGATGTGAGAATAACNCCAGCTGCCGGCAAGCACACCTCGATNCNATN 325
529 TCTGATTGTCGTCTTGGCTTGGCTTAATTGGTGTGTGTGTGTGTGTTGC 578
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326 ACTNATT.....TAACTATAATTGATTTTCTTGGGTTTCTGC 364
579 AGGGCAAGGTGGCGCTCATGTCCACGGGCAGCTTGACCCAGCTGCACGTC 628
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365 AGGGCAAGGTGGCGCTGATGTCGGCAAAGAGCATGCACCAGCTGCACATT 414
629 TTCATCTTCGTGCTCGCGGTCTTCCATGTACCTACAGCGTCATCACCAT 678
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415 TTCATCTTCGTGCTCGCCGTGTTCCATGTTACCTACTGCATCATCACCAT 464
579 AGCTCTAAGCCGTCTCAAAGTGAGCCTTTGCTTCT.....TCTTCTTCTT 723
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724 CTTTTACC.....GCACGTCTGTCTGTACAGGCGTACCTACCTGTTCA 765
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808 TCCTCTCCTCCTG....CAGATGAGAACATGGAAGAAATGGGAGACAGAG 853
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609 TTGATCTTTCTTGGTTTTAGATGAAGAAATGGAAGAAGTGGGAGTCACAG 658
854 ACCACCTCCTTGAATACCAGTTCGCAAATGGTCAGGATCCCCACTCTG 903
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659 ACCAACTCATTGGAGTATCAGTTCGCAATCGGTAGTG.....AATTAA 701
904 CAATCTCCC...CTTCTTCGAAACCAAACC...TGATGATCCATTTAAA 946
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947 GACGCAGGCACGATCAGAGTGAGTGAAC TGATGTATGTTTATTTTGTG 996
|| | | |||| || | |||| |
752 GAGGAGGAGCAAATCAG.CTGAAAAATATGATCGA..... 785
997 TCCTTTCAGATCCTGCACGGTTCGGTTCACGCACCAGACGTCGTTTCGTG 1046
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786 TCCATGCAGATCCTTCACGATTCAGGTTACGCATCAGACGTCGTTTCGTG 835



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 1024 GGGTCCGTCACCAAGGTGGACTACCTGACCATGCGGCAAGGCCTTCATCAA 1073
 1266 CGTACGTGC...CTCCCCCTTCTAGCTCCGCCATTGCTGCCGCGATGTAG 1311
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 1123 AAGACCAGGTTTTTTTTTTTCCGAGTTGTGCAT.TGAAGTTAATG..... 1165
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 1166 .GTTTTAGCTTC...TTCTCTTTTGCAGGCGCCATTGTGTCGAGAATAGC 1211
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 1427 CTTGTACTCTTCTCGATATCCACGGTA..ATCCTTGTCT...ATT 1469
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 1520 CCATCGATTTTTTTTTCAACTT.TTCCCCGCGTGTAGGTCTTGGCACACT 1568
 1798 CATCTGGATTTCTTTCATCCCTCTCGTGGTAAGTGC.AGATTCTCC.AT 1845
 1569 TATTTGGATCTCTTTTGTTCCTCTCATCGTAAGAGCGAAATTTCCCCTGT 1618



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1717	TTGTCTCAGATCGTCTTGTTAGTTGGGACCAAGCTAGAGATGGTGATCAT	1766
1979	GGAGATGGCCCTGGAGATCCAGGACCGGGCGAGCGTCATCAAGGGGGGCC	2028
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1867	GTCTTGTTCTTCATACACCTGACACTCTTCCCATGTACATGTTTAAACC	1916
:		
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2211	ACACCTGGTCTGAAGAAATGCTTCCATGAAATATTTGGCTGAGCATCGT	2260
2294	GAAGGTGGTGGTGGGGCTAGCTCTCCAGTTCCTCTGCAGCTATATGACCT	2343
2261	GGAAGTCATTGTGGGGATCTCTCTTCAGGTGCTATGCAGCTACATCACCT	2310
2344	TCCCCCTCTACGCGCTCGTCAACACAGGTAATAAAACCGTCCAGGAA	2389
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Figure 6A

295 GAGCTCATGCTGGTGGGCTTCATATCCCTGCTCCTCATCGTCACGCAGGA 344
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1 GAGCTCNTGCTGGTGGGCTTCATATCCCTGCTCCTCATCGTCACGCAGGA 50

345 CCCCATCATCGCCAAGATATGCATCTCCGAGGATGCCGCCGACGT CATGT 394
| | | | | | | | | | | | | | | | | : | |
51 TCC...CGTCTCCAGGATCTGCATCTCCAAGGAGGCCGGCGANAANATGC 97

395 GGCCCTGCAAG.....CGCGGCACCGAGGGCCGCAAGCCCA..... 430
| | | | | : | | | | | | | | | |
98 TCCCGTGCAAGCCTTACNACGGCGCCGGCGGTGGCAAAGGCAATGACAAT 147

431GCAAGTACGTTGACTACTGCCCGGA 455
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148 CACCGGAGGCTTCTCTGGCTCCAAGGCGANAGCGANACCCACCGCCGGTT 197

456 GGTGAGCAGCAGAGCCCGGACCAG..... 479
| | | | | | | : |
198 CCTG.GCTGCCCGGCCGGANTGGACGTCTGCGCCAAACAGGTGAGCACC 246

480 CAGCTTCACGATGATGAAGAAA.TCAATACCGAACTTTTCTTGTTTTCT 528
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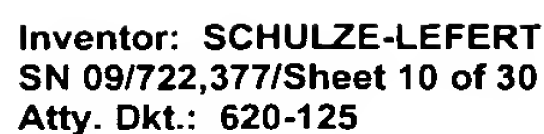
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:
:

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877 C..... 877

:
:
:

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| | | | | | | | | | | | | | | | | | | | | |
1323 CAACCTGTCCAATTGTGATGTACAGTACCTCCAAACTTAA.....TTA 1365

1905 AAATGTCAATTGTCGGTGCGTCTTCC.....TCAACAGATCCTCTTGTGT 1949
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1366 ACATGTCATTTGCTGAT..GTCTTGCGTGTAACATTAGATCCTCTTGTGG 1413

1950 GTTGGAAACCAAGCTGGAGATGATCATCATGGAGATGGCCCTGGAGATCCA 1999
| | | | | | | | | | | | | | | | | | | | | | | | | | | : | | | | | | | | | | | | | | | | | | |
1414 GTTGGGACCAAGCTGGAGATGGTGATCATGGAGATGGCCCAGGANATCCA 1463

2000 GGACCGGGCGAGCGTCATCAAGGGGGCCCCCGTGGTTCGAGCCCAGCAACA 2049
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1464 TGACCGGGAGAGCGTCGTCAAGGGTGCTCCCGCCGTCGAGCCCAGCAACA 1513

2050 AGTTCTTCTGGTTCCACCGCCCCGACTGGGTCTCTTCTTCATACACCTG 2099
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1514 AGTACTTCTGGTTCAACCGGCCTGACTGGGTCTCTTCTCATGCACCTC 1563

2100 ACGTTGTTCCAGAACGCGTTTCAGATGGCGCATT TTTGTGTGGACAGTGGT 2149
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1564 ACACTCTTCCAGAACGCGTTTCAGATGGCTCATTTTCGTGTGGACAGTGGT 1613

2150 ACGCCACCGATGA ACTTGTCAGTTAACATGGG..... 2181
| | : | | | | | | | | | | | | | | | : | |
1614 A...CNTACAAGTACTTGTCACTTCACTTANGCTAACTCCAACAAACGAA 1660

:

2182TGTC AAGGCACC GAGTGCCGCTGATGAACTGCTCTGACGGAG 2223
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1711 GACACAAA ACTCAATCCAACGCGCGGTAGCAAACGAACGTTTTTCCGTAC 1760

2224 ATTTAC.....TTG 2232
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1761 GTTTTCGTCCGCTTTCGCCCCATCCCAGCCCAAATTCGTTGACGTTGTTG 1810

2233 TGTTGTAGGCCACGCCCGGCTTGAAGAAATGCTACCACACGCAGATCGGG 2282
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1811 CATCGCAGGCCACGCCCGGCTTGAAGAAATGCTACCACGAGAAAATGGCA 1860

2283 CTGAGCATCATGAAGGTGGTGGTGGGGCTAGCTCTCCAGTTCCTCTGCAG 2332
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1861 ATGAGCATCGCCAAGGTCGTGCTGGGGGTAGCCGCCCAGATCTTGTGCAG 1910

2333 CTATATGACCTTCCCCCTCTACGCGCTCGTCACACAGGTAATAAAACCGT 2382
: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1911 NTACATCACCTTCCCGCTNTACGCGCTCGTCAC..... 1943

:

2433 AATCATCTGTGTGTGCTGGCTTTGTATGCAGATGGGATCAAACATGAAGA 2482
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1944GCAGATGGGCTCACACATGAAGA 1966

2483 GGTCCATCTTCGACGAGCAGACGTCCAAGGC.GCTCACCAACTGGCGGAA 2531
| | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1967 GAAGCANCTTCGACGAGCAGACGGCCAAGGCGGCTGACCAACTGGCGAAA 2016

2532 CACGGCCAAGGAGAAGAAGAAAGTCCGAGACACGGACATGCTGATGGCTC 2581
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
2017 GATGGCCAAGGAGAAGAAGAGGCCCGAGACGCGGCCATGCTGATGGCGC 2066

2582 AGATGATCGGCGACGCAACACCGAGCCGAGGCTCGTCGCCGATGCCGAGC 2631
| | | | | | | | | | | | | | | | | | | | | | | | | | | : | | | | | | | | | | | | | | | | | |
2067 AGATGGGCGGCGGCGCGACGCCGAGCGTCGGCTNGTCGCCG..... 2107



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Figure 6D

```
2632 CGGGGCTCATCACCCGTGCACCTGCTTCACAAGGGCATGGGGCGGTCCGA 2681
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2108 .....GTGCACCTGCTCCACAAGGCCGGGGCGCGGTCCGA 2142
      .
2682 CGACCCCCAGAGCGCGCCACCTCGCCAAGGACCCAGCAGGAGGCTAGGG 2731
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2143 CGACCCCCAGAGCGTGCCGGCGTCCCCGAGGGCCGAGAAGGAAGGCGGCG 2192
      .
2732 ACATGTACCCGGTTGTGGTGGCGCACCCGGTGCACAGACTAAATCCTAAC 2781
      | || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2193 GC.....GTGCAGCATCCGGCGCGCAAGGTACCTCCTTGT 2227
      .
2782 GACAGGAGGAGGTCCGCCTCGTCGTCGGCCCTCGAAGCCGACATCCCCAG 2831
      ||| || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2228 GACGGGTGGAGGTTCGCCTCGTCGCCGGCGCTCGACGCTCACATCCCCGG 2277
      .
2832 TGCAGATTTTTCCTTCAGC.....CAGGGATGAGACAAGTTTCTG 2871
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2278 TGCAGATTTTGGCTTCAGCACGCAACGTTGACCGATCAGACAAGTTCCTT 2327
      .
2872 TATT 2875
      | |
2328 TTTT 2331
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Figure 7

	GGCTGCTCCGCCAGCAAACAGACACACAGCAGCGTACCTGCGT	
	ACGTAGCGTGCGCTTTCTTTTTTTTCTTTTCGCTCTCTTGTGCTCCGCCGCCACG	
	TCGATAGCCGGCCACGGCCAGGCACCTCGCGGTTGCGTCGCGTGCATCTGCGTGTGCGTA	
	CCTGGTAGAGGCGGCCGCTGCTTGTCTCCGGGCAAGGAAGGAGGTTGCGGCGGTCGACCG	
helix I	M S D K K G V P A R E L P E T P S W A V	20
	ATGTCGGACAAAAAGGGGTGCCGGCGGGAGCTGCCGGAGACGCCGTCGTGGGCGGTG	60
	A V V F A A M V L V S V L M E H G L H K	40
	GCGGTGGTCTTCGCCGCCATGGTGTCTGCTGCTCCGTCATGGAACACGGCCTCCACAAG	120
helix II	L G H W F Q H R H K K A L W E A L E K M	60
	CTCGGCCATTGGTTCCAGCACCGGCACAAGAAGGCCCTGTGGGAGGCGCTGGAGAAGATG	180
	K A E L M L V G F I S L L L I V T Q D P	80
	AAGGCGGAGCTCATGCTGGTGGGCTTCATATCCCTGCTCCTCATCGTCACGCAGGACCCC	240
helix III	I I A K I C I S E D A A D V M W P C K R	100
	ATCATCGCCAAGATATGCATCTCCGAGGATGCCGCCGACGTCATGTGGCCCTGCAAGCGC	300
	G T E G R K P S K Y V D Y C P E G K V A	120
	GGCACCAGAGGGCCGCAAGCCAGCAAGTACGTTGACTACTGCCCGGAGGGCAAGGTGGCG	360
helix IV	L M S T G S L H Q L H V F I F V L A V F	140
	CTCATGTCCACGGGCAGCTTGACACAGCTGCACGCTTCATCTTCGTGCTCGCGGTCTTC	420
	H V T Y S V I T I A L S R L K M R T W K	160
	CATGTCACCTACAGGTCATCACCATAGCTCTAAGCCGTCTCAAAATGAGAACATGGAAG	480
helix V	K W E T E T T S L E Y Q F A N D P A R F	180
	AAATGGGAGACAGAGACCACCTCCTTGAATACAGTTGCGAAATGATCTGCACGGTTC	540
	R F T H Q T S F V K R H L G L S S T P G	200
	CGGTTACGCACCAGACGTCGTTGCTGAAGCGCCACCTGGGCTCTCCAGCACCCCTGGC	600
helix VI	I R W V V A F F R Q F F R S V T K V D Y	220
	ATCAGATGGGTGTTGGCCTTCTTCAGGCAGTTCTTCAGGTCAGTCACCAAGGTGGACTAC	660
	L T L R A G F I N A H L S Q N S K F D F	240
	CTGACCTTGAGGGCAGGCTTCATCAACGCGCATTGTGCGAAAACAGCAAGTTCGACTTC	720
helix VII	H K Y I K R S M E D D F K V V V G I S L	260
	CACAAGTACATCAAGAGGTGCGATGGAGGACGACTTCAAGGTCGTCGTCGGCATCAGCCTC	780
	P L W G V A I L T L F L D I N G V G T L	280
	CCGCTGTGGGGTGTGGCGATCCTCACCCTCTTCCTTGACATCAATGGGGTTGGCACGCTC	840
helix VIII	I W I S F I P L V I L L C V G T K L E M	300
	ATCTGGATTTCTTTCATCCCTCTCGTGATCCTCTGTGTGTTGGAACCAAGCTGGAGATG	900
	I I M E M A L E I Q D R A S V I K G A P	320
	ATCATCATGGAGATGGCCCTGGAGATCCAGGACGGGCGAGCGTCATCAAGGGGGCCCC	960
helix IX	V V E P S N K F F W F H R P D W V L F F	340
	GTGGTCGAGCCCAGCAACAAGTTCTTCTGGTTCCACCGCCCCGACTGGGTCTCTTCTTC	1020
	I H L T L F Q N A F Q M A H F V W T V A	360
	ATACACCTGACGTTGTTCCAGAACGCTTTCAGATGGCGCATTTTGTGTGGACAGTGGCC	1080
helix X	T P G L K K C Y H T Q I G L S I M K V V	380
	ACGCCCCGGCTTGAAGAAATGCTACCACACGCAGATCGGGCTGAGCATCATGAAGGTGGTG	1140
	V G L A L Q F L C S Y M T F P L Y A L V	400
	GTGGGGCTAGCTCTCCAGTTCCTCTGCAGCTATATGACCTTCCCCCTCTACGCGCTCGTC	1200
helix XI	T Q M G S N M K R S I F D E Q T S K A L	420
	ACACAGATGGGATCAAACATGAAGAGGTCCATCTTCGACGAGCAGACGTCCAAGGCGCTC	1260
	T N W R N T A K E K K K V R D T D M L M	440
	ACCAACTGGCGGAACACGGCCAAGGAGAAGAAGAAAGTCCGAGACACGGACATGCTGATG	1320
helix XII	A Q M I G D A T P S R G S S P M P S R G	460
	GCTCAGATGATCGGCGACGCAACACCGAGCGGAGGCTCGTCGCCGATGCCGAGCCGGGCG	1380
	S S P V H L L H K G M G R S D D P Q S A	480
	TCATCACCCGTGCACCTGCTTACAAGGGCATGGGGCGGTGCGGACACCCCCAGAGCGCG	1440
helix XIII	P T S P R T Q Q E A R D M Y P V V V A H	500
	CCCACCTCGCCAAGGACCCAGCAGGAGGCTAGGGACATGTACCCGTTGTGGTGGCGCAC	1500
	P V H R L N P N D R R R S A S S S A L E	520
	CCGGTGCACAGACTAAATCCTAACGACAGGAGGAGGTCCGCCTCGTCGTCGGCCCTCGAA	1560
helix XIV	A D I P S A D F S F S Q G *	
	GCCGACATCCCCAGTGAGATTTTCTTTCAGCCAGGGATGAGACAAGTTTCTGTATTCA	
	TGTTAGTCCCAATGTATAGCCAACATAGGATGTGATGATTTCGTACAATAAGAAATACAAT	
	TTTCTACTGAGTC	



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Figure 8A

1 GAATTCAATT AAGGACAACA ACGGATGATA GGCTTAAGCT AGAGAGGATT
51 CATATGGATT AATTAAGTGT ACTTAAGTTG AGGTAAACT CTATCGATTG
101 CTTTGGACAC CGGCTCTCCC ATGATCTGCC AAGTTGAGCC GGCCTACCTA
151 ATTTTCTTCG AAAGCACACA ACAAACGAAG GTAACCACTA ATCTAGACAC
201 CACGCCTAAG TTATCAATTA CTACTCTAGT CTCGCGTAGA AACTTCATTC
251 TTTATGGAGA GTGCTAGTAC TAGAGTACTT AATATAATAG TAAGCGACAA
301 ACCCAGGACG ATGAGAATGT ACCTCACTTA CGTAAGTCAA TTAAGTCGAA
351 AAGGAAATCT TGAACACTTA CTTTATTAAA GAAGTATTCC CCGAGGTACA
401 GGAGAGGAGA GCACGCCAAT AACTCCAGCA CTCCTCCGAA ACCTTTCTCA
451 CTCTCTACCC TTTTCTCCA CACAATAAA ATGATGTCTA ATGTATGAAA
501 GTGAGTTGTA CTCTATTTTG TTGTGTGTTT GGAAGTGAAA TTAGCTCATC
551 CTTTTATAGC AGCTTAATGG TCGGTTGTAG GTTGGTAGTT AAGTCGGTAA
601 AACTCACA CCACCATCGT CAACCAATAG GAGATCGCCA CATGATCGAA
651 AGCTGACAGT TAGGGGTGCC AACCTGTTT TGTCCGAACC AAGCAAACAA
701 CCTCTAGCTA GGACCTCTCT TCTATGTCTG ACAAGTCGGC CCATATGGCG
751 GTGCACTATG GATTAGGTCA ATTTAGTCG TTTTGGACTG TCATGTGGGC
801 CCTTCCAATC CTTGTGCTCC CATATGATTG GTCGAAGGTA CATTTAATTC
851 CTGGGTGAGT GCTAGAACTA ATATGATAGA TGTGCTCGGG CTCCTGGGAA
901 AGAGGCCACT TGACATACTT GGGGTAGTGC CCCAAGGGTA TTCCCTATCG
951 CTTTTTCATA ATTTTCTCTC TCCAAAATCG GACGGAAACA ATAAAAAGA
1001 GAGGCGATGT TCATCGGCAA ATATCTATTT TTTTGATAGT GTCTTCCCTT
1051 AAAACTTGAT TTTTGCGAAG ACTTCCGGCT AAAACCATGA AATCAGAGTT
1101 CCTTGTAACA AATTTAATTT GCCTAAATAC AAAAAAGATC GAATGGAGAT
1151 AGCATTAAAC TTGCTCCATA CGAATCATAT TAGTTGGACC GTAACTCATA
1201 GAAAAAGTTG CAAGTTGGTT GACCTATCAA CCCTCTTATG TTGACCCGTA
1251 AACCTGTTA TGCATTAAGG ATTAAGTACC CGGCAGATCG TCACTACTCA
1301 CGAATGCACA AATTTCCGGT ACGTAGGATG GGATGAGTTG GTCAGAAACG
1351 GGCTCACCAC GTCGCCCAAC CTGCCGCGAT CGAGCCATTG GCCGGCGATG
1401 CACGCGCTTT GACACAGCCG CCCGCCGCC CCCGGCCCGC CCCCCTCTT



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Figure 8B

1451 TAATAAAAAC CGGCCGCCCC CTGTCAAAGG TGTCAAAGTG TCAAGTGCAT
1501 CAGAGCTAAG CTAGCGGTCA CCCAGTCAGC TCACCCCGAG ACGCACCAGG
1551 GGATCTATCG GATCATGGCA GGTGGGAGAT CGGGATCGCG GGAGTTGCCG
1601 GAGACGCCGA CGTGGGCGGT GGCCGTCGTC TCGCCCGTCC TCGTGCTCGT
1651 CTCCGCCGCC ATGGAGCACG GCCTCCACAA CCTCAGCCAT GTACGCGCGC
1701 GCGCACGCGG TGTGCTCATC TCTCGAGTTA ATTTGGTTGT TGTGTTGTT
1751 GTGTTCTTGT GACATCTCAA TTAACATCCG ATCCTGGTCG ATCGATCGCC
1801 CTGTGGTGGC GCTACTGCTT GCATTGCAGT GGTTCGCTAG GCGGCAGAAG
1851 AAGGCCATGG GCGACGCCCT CGACAAGATC AAAGCAGGTC ACCCTCAGCC
1901 TCAGCTCACC CTCAGCCTCC ATCTCTAAAT ATTTGACGCC GTTGACTTTT
1951 TTAAATATGT TTGACCATTG GTCTTATTTA AAAAATTTAA GTAATTATTA
2001 ATTCTTTTTC TACCATTTGA TTCATTGCTA AATATACTAT TATGTATACA
2051 TATAGTTTTA CATATTTTAC TAAAGTTTTT AAATAAGACG AATGGTCAAA
2101 CATGTTTAAA AAAGTCAACG GCGTCAAACA TTTAGGAAGA AGAGAATATT
2151 ATATTGCTGC TCCCCTCTAG CCACTTTGCT GCCTCCCTCG TCATTTTTC
2201 AAGTATTTTA CGCAAGACTG GGTCTCCAA ATCAAACGTC ACAAATAAGC
2251 CATTTATAGT TTCCTTTCGC TTTTAAAGGG GGGACTACTT GTATTTAATC
2301 ATGGAGGAAA CTACCAGTCG GATGTCCGAT TACTTAAAAA AAAATTCGGG
2351 GGACTAATTT TTTTGGCTGA TCATCGGTGA AATATTAGGT TATATATGTT
2401 GAAAAAAAAT CAGCCACAAA CAATGAAATA TTTTGTGAAA CACATATTAG
2451 ACACGTTGAA ACGTATCATT GTTACGTATA AAACATCGAA TGTTAACAGA
2501 TTAAACATA TGTTTTTTTT TAATCAGAAT ATAATCATGC GATATATTAT
2551 TGTAAAGATA TAATTACAAC GAATACAACA GTGCGATCGG ATTATATATA
2601 TATTAGTAGT TTAAGAGAAA AATCATTTTG AAGATTACTA GATACATACA
2651 CGTATAGATG GATGAAGTGG AGAGAGATTA GAGATAAGTA GTTATATGAA
2701 TTTTGTGAAA CACACTTAAG ACATATGTTC AAACATACTG CTATTATGTA
2751 TGAAATATTG AGTTTAAACG GTTTAAAACA CATATTCTTT TAATTAGAAT
2801 GTAATAATGT GATATCTTGT TGTAATAATT AATTACATCT AATATAACGG
2851 TGTGATTAGA TTGTATGTTG GATAACATGC CCATCGGTTG GCTTATTTAG
2901 GGAATAAGCC AAATGGTATA TTTGCAAACG AAAAATAATT TGTAAATAAA
2951 ACTTTTATGT ATGTATTCTT AACGATCTAG CAGCAAAGGC TGAAAAATAA
3001 ACTTCGATGA AAAATCTCAA AATCAACTCT TAAAATTTAA ATTTTGCTT



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Figure 8C

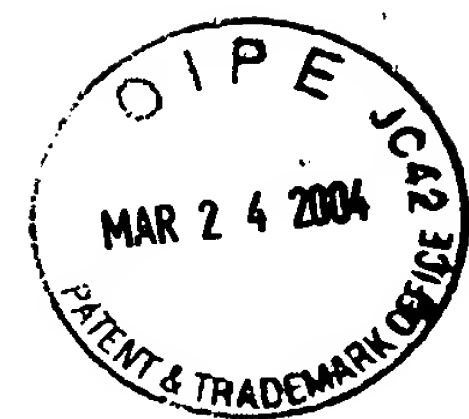
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3101 AGAGGAAAAG GAATAAACTA ATAGCTAAAT TATTGCATGC ATGTAGCGAT
3151 TTGAGGACGA CCGAGTTGTT TTGTCTGGAT CAGCCGACCG AGACAGAGCA
3201 ATCTTCTTTA ATCATAAATA ACCAGAAAAA CCATACCAGT TCATCACAAT
3251 GGACCGAGTC AGAGTCATTA CATATTTTTC ATTGTTGCGC ACAGGATTCA
3301 CCATGTTCTT ATGGGAAATA TTTTAACTC TCAAATGGTT ATGATTTTGA
3351 ACTCTCATTT TTGAGAGAGA ATTAACAAGC GAGCGAGCAA TCAGGCCAAA
3401 AAGGGAGAAA GAAAATTATT TTTGTTAATT TTTTTTTAAG GTAGGGTGGA
3451 GGAGTCATTA CATGATTTTT TTTTATATTC CCTCGTTGAT TATATGCTGT
3501 TCAAATGGTT ATGATTTTTT TAAAAGATAA CAACAATACA AATTAGTATG
3551 TGATAGATCA TTTCACGAGC ATATAGGATT AAATTTAACT TCTGTAAATT
3601 ACAAACAAA CAAGTTTAAC TGTTAATATA CATTAAATTT GTTTTTTTCA
3651 ACTTAGGAAT TGAATTTTAT GTATATATTT GTAAAATGAT ATATTAATTT
3701 ATTTTTTTAA AAAAATAATT ATTTAGATAA CACGCAAAC AGAAAACCAC
3751 CGCAGAAGTT CTCATATTTT TTGTCCTATC TGCACTTGCA GAGCTGATGC
3801 TGCTGGGCTT CATATCCCTG CTTCTCACCG TGGCACAGGC GCCCATCTCC
3851 AAGATCTGCA TCCCCAAGTC GGCTGCCAAC ATCTTGTTGC CGTGCAAGGC
3901 AGGCCAAGAT GCCATCGAAG AAGAAGCAGC AAGTGGTCGC CGGTCCTTGG
3951 CCGGCGCCGG CGGCGGGGAC TACTGCTCGA AATTCGATGT GAGAATAACA
4001 CCAGCTGCCG GCAAGCACAA CCTCGATGCA ATAACTAATT TAACTATAAT
4051 TGATTTTTCT TGGGTTTTCT GCAGGGCAAG GTGGCGCTGA TGTCGGCAAA
4101 GAGCATGCAC CAGCTGCACA TTTTCATCTT CGTGCTCGCC GTGTTCCATG
4151 TTACCTACTG CATCATCACC ATGGGTTTAG GGCGCCTCAA AGTGAGTTTG
4201 TCGTTCTGTC CCTCATGCAC ATGTTTTCTC TAGTTCTAGC AAGATTGTCA
4251 GTCCTTCAA TGGATTGTTT CGACAAGAAA CCAATTTAT TAATTTGCCA
4301 GTAAATATAT AATAATTGAT CTTTCTTGGT TTTAGATGAA GAAATGGAAG
4351 AAGTGGGAGT CACAGACCAA CTCATTGGAG TATCAGTTCG CAATCGGTAG
4401 TGAATTAAGA ATCTCCCTAA CTATTTTATT TCAGAACCTT TATGATAATG
4451 TCTTGAAAGA GGAGGAGCAA ATCAGCTGAA AAATATGATC GATCCATGCA
4501 GATCCTTCAC GATTCAGGTT CACGCATCAG ACGTCGTTTC TGAAGCGGCA
4551 TCTGGGATCA TTCTCAAGCA CCCCTGGGCT CAGATGGATC GTGAGTTATC
4601 AATCTCCGAA TACATGCTTG TTTTTTATTC TTGCAACTGG CCTAGCTGTT



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Figure 8D

4651 CCAATTCAAT CCATATTTTT TGAAAAAAAA AATATTCATG CCGTGTTTGT
4701 TGTTAGGTAG CATTCTTCAG GCAGTTCTTT GGGTCCGTCA CCAAGGTGGA
4751 CTACCTGACC ATGCGGCAAG GCTTCATCAA TGTATATACT AATCAAACCT
4801 GACCAATTCA ACATTGATGA TGCAAACAGA GACCAGGTTT TTTTTTTCGA
4851 GTGTGCATTG AGTAATGGTT TTAGCTTCTT CTCTTTTGCA GGCGCATTG
4901 TCGCAGAATA GCAAGTTCGA CTTCCACAAA TACATCAAGA GGTCTTTGGA
4951 GGACGACTTC AAAGTTGTCG TTGGCATCAG GTCCGTCCTC GCTTTATTAA
5001 TTATAGGACT CTTATATTCA ACATTTTTTT TATAAAGAAA CATATTTAGT
5051 CTCCAGTTGT GTATGTGTAT GTGGATCTTG ACACATTTGG CTGGTTTTGC
5101 AGCCTCCCTC TGTGGTTCGT CGGAATCCTT GTACTCTTCC TCGATATCCA
5151 CGGTAATCCT TGCCTATTT CATTCTTTTT TTTACTCTCA AAACCTTGTT
5201 CTGAATTGGT CTTATAATCA CCATCGATTT TTTTCAACT TTTTCCCCGC
5251 GTGTAGGTCT TGGCACACTT ATTTGGATCT CTTTGTTTCC TCTCATCGTA
5301 AGAGCGAAAT TTCCCTGTCC AAAGAAACAG TTAACATAAT TAATTATGCT
5351 TTAATTTATC ATGAAAATTA ATATGATCAT ATAACATAAT AACAAACATT
5401 CATGTGAATG CCACCGTTGT CTCAGATCGT CTTGTTAGTT GGGACCAAGC
5451 TAGAGATGGT GATCATGGAG ATGGCCCAAG AGATACAGGA CAGGGCCACT
5501 GTGATCCAGG GAGCACCTAT GGTGAACCA AGCAACAAGT ACTTCTGGTT
5551 CAACCGCCCT GACTGGGTCT TGTCTTCAT ACACCTGACA CTCTTCCATG
5601 TACATGTTTA AAACCTAAAC CTTGCTGCTC AACTACAAAT AGTACTTTAT
5651 CTTTCACAAT TAACACCTAA TTAACATAA TAGCATCCAT CCATTTGTGG
5701 CTAATGATCG ATGGGACGAC GGATCGATCA TCACCAGAAC GCATTCAGA
5751 TGGCGCATTT CGTATGGACT ATGGTGTGTA TGCTACTTGC TTAGTTGTTG
5801 CCATTATCAG TTCTTAAGCA AATTAAGTGT GATGCATGCA CTGACTAATG
5851 AGACAAAAAA TGACACAGCT TGTTTCATCGA TCTGGTTGTT TTGTGTGTGA
5901 CAGGCAACAC CTGGTCTGAA GAAATGCTTC CATGAAAATA TTTGGCTGAG
5951 CATCGTGGAA GTCATTGTGG GGATCTCTCT TCAGGTGCTA TGCAGCTACA
6001 TCACCTTCCC GCTCTACGCG CTCGTCACAC AGGTGAACAA GCCATTCACA
6051 AATTCTATTA GCCGTTTCTT AATTGATGAC ACTGTTAATT TTTAGACACA
6101 CGTTTTGACC ATTTGTCTTA TAAAAATAT TTATGTAATT ATCATTGAG
6151 TTGTTTTATC ACTAAAAGTA CTTTTTAAAT AATTTATATT TTGCATTTGT
6201 ACAATTCTTT TAATAAGATA ATGGTCAAAC ATGTGTCCAA AAGTTAACAG



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Figure 8E

6251 CATCATCTAT TAAGAAAAGG AGGGGTTTTT TTTTTTTGGA ATTTTGCAAA
6301 ATTTGTTCAA AATCAGTCCA AAACCTTTTT TTTTTTCGAA ATTTCAGTTT
6351 CACTACCAGT CCCCATAAAA TGTCTTTTCT TTATTTCCAC AAGATTGAAC
6401 CCATGAGATG CCCTTTGTGT TGGTATGTGT TTTGGCCATC ACTTGCAGAT
6451 GGGATCGAAC ATGAAGAAGA CAATTTTCGA GGAGCAAACG ATGAAGGCGC
6501 TGATGAACTG GAGGAAGAAG GCGATGGAGA AGAAGAAGGT CCGGGACGCC
6551 GACGCGTTCC TGGCGCAGAT GAGCGTCGAC TTCGCGACGC CGGCGTCGAG
6601 CCGGTCCGCG TCGCCGGTGC ACCTGCTGCA GGATCACAGG GCGAGGTCGG
6651 ACGACCCGCC GAGCCCAATC ACGGTGGCCT CACCACCGGC ACCGGAGGAG
6701 GACATGTACC CGGTGCCGGC GGCGGCTGCG TCTCGCCAGC TGCTAGACGA
6751 CCCGCCGGAC AGGAGGTGGA TGGCATCCTC GTCGGCCGAC ATCGCCGATT
6801 CTGATTTTTC CTTCAGCGCA CAACGGTGAC GGGGGCGATC GGTTTCTGTA
6851 TTGATGCTGT ACCAAACATA GGAGTTTAAT ATATATATAA TTGTTACGGT
6901 AAAATCTAAT TATTGTGCGC GCACTTATAT TAGTCTTATA GCGCGACTGG
6951 TTCGTGATTA GACAAGGTGA TGCATGCTGT TTAGTTATAA AGGATATCAG
7001 CGCAGCTAAA AAAACTTACT CCCTACTTAA TAGATGACCT CGTTGATTTT
7051 TAACATTATT CGTCTTATTT AAAAAATTTA TGCAAATGTT TAAAACATAA
7101 ATCATGCTTA AAGTACTTTT AGTGATAAAA CAACTTACAA CAAAATAAAT
7151 TATAGTTACC TAATTTTTTT TAATAAATCG AATGG



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Figure 9A

1 TTATACCATG TGAGAAAGGC TGAAGCATA TGCTCTTAGC AGGGACGCGT
51 GCATGTTTAT ATAGGAGGCA TAAGCCGAAG AGATATACAT GAGGAGAGGT
101 TTAAGATCAG TCTATCTTAT TTACAGTTTA AACACAAGGA GATAGAAAGA
151 GATCCTAACC TACACATGTT ATACAAGTCA CGTATAATAC AAGAGTTATT
201 TCGTCTAACA CCCTCCCCTC TGATATGATA AGTCGCCGGG AGAGAGAGAG
251 AGTGTGTGGC TGCCCTCGCT GCACTGCACG CACATGTTTA CTTCTCCGAC
301 TGAAACCACG GTGAAACCGG CGGCGGTGTC GCACTCCCCT GACTTTCCTC
351 GCCGGGGTCC CGTCCGGACA ATTAAACCGT CTGTACCTGC CGGGCGTCGA
401 CCCGATCGTG ATGTGGCGCC GCTTTGTCTG CAGCGAGCTG CGTGGCCGAT
451 GGCAACAAAA CTGCGGTCAC ATACATGCAT ACCCCGCATA CCCCAGCGCT
501 CACCAGTAAG TAGGCTGTGG TCGGGACCA CGGGCTCGCC GCCATTCATG
551 CCATGCATGG GCCACCCGCC GCGGAAACCG CGGCGCTGCT GCCTGCCACC
601 CCGCCGCCGT TGACGAAGAC TTCGCCCGGC CATCCATAAA AGCATGCATG
651 GCTTGCTCTC ACCGGTCCGG CCACACACAC CACACTTCAC TTCGCCATTC
701 GCACCACCGA GAGCGTAGCG TAACGTGTGT TTGAAGTCCT ACCATTAATT
751 TTGCTGGATC GATGGCTGGG CCGGCGGGAG GTCGGGAGCT GTCGGACACG
801 CCGACGTGGG CGGTGGCGGT AGTCTGCGCC GTCATGATAC TCGTCTCCGT
851 CGCCATGGAG CACGCGCTCC ACAAGCTCGG CCACGTACGT GCTCTCGGTT
901 CACTAGTGCT TAACTGTTTT TGATGTTTTT GGGCGTGTTT GGTAGCCTGC
951 ATGGAGAGTG TATGAGCCCA AAAGTTCCT CCCCAGCCCA CTTTTCGCTG
1001 TTTGGTAGGG TGTATGGGCT GAGGAGAGCA TGCATCAACT GATGCAAAAA
1051 GGGCCTCAGC ATAGCTGAGC CCAGCACCCC CGCAGAGGCG AGCTGAGGCG
1101 AGTTATGCTG AGCCCATGCA CCCTCGCCCC GTCGCCCCGT CGCCCCGTCG
1151 CTCCCCCCT GCACCTCTTC CTCCTCCCTC TTCCTACCAA ACACAGTCTC
1201 ATCCAAACAT GTAACAACAC ATGCATGACC ACCAAACAAC TGAAGATGAA
1251 TGTATTCATC ATGTCTATAC TTACCATGCA TCAACAGGGA ACAACTATGC
1301 TAGGGTGAGA ACAGCTGCCA AACACACCCG TGCACCTACT CATGCTGTGC
1351 CGGCGCTGGC GTACGTGTGC AGTGGTTCCA CAAGTGGCGC AAGAAGGCCC
1401 TGGGGGAGGC GCTGGAGAAG ATGAAGGCGG AGCTCATGCT GGTGGGCTTC



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Figure 9B

1451 ATATCCCTGC TCCTCATCGT CACGCAGGAT CCCGTCTCCA GGATCTGCAT
1501 CTCCAAGGAG GCCGGCGAGA AGATGCTCCC GTGCAAGCCT TACGACGGCG
1551 CCGGCGGTGG CAAAGGCAAG GACAATCACC GGAGGCTTCT CTGGCTCCAA
1601 GGCGAGAGCG AGACCCACCG CCGGTTCTTG GCTGCCCCGG CCGGAGTGGA
1651 CGTCTGCGCC AAACAGGTGA GCACCTAGCG TCGCCACAAA CCACAAACTA
1701 GCTAATGAGC ATGGACCTGA ATTTCTTCTC TTCTTGGCTT GGCTTGACTA
1751 AATTGGTTGT GCAGGGCAAG GTGGCGCTGA TGTGAGCGGG AAGCATGCAC
1801 CAACTGCACA TATTCATCTT CGTGCTCGCC GTCTTCCACG TCTTGACAG
1851 CGTCGTCACC ATGACCCTAA GCCGTCTCAA AGTGAGCATC ATACTCGAGC
1901 TGTTTGTCAA TAATCCTTGG TTTCCAATCC AATTCCAAAG CTGGCACTGA
1951 TCCTGCTCCG GCTTCCTGCA GATGAAGCAA TGGAAGAAGT GGGAGTCGGA
2001 GACCGCCTCG CTGGAGTATC AGTTCGCGAA TGGTCAGCTT CAACTTTTCT
2051 TACTGAAACC GGATGCATTT ACAACAAACG CACGCACGAT CAATCATCAC
2101 AGTGTGAGCC GATACGTTGA ACCGATTGAA TCCTCGCAGA TCCATCGCGG
2151 TGCCGGTTCA CGCACCAGAC GACGTTGGTG AGGCGGCACC TGGGCCTCTC
2201 CAGCACCCCC GCGGTCAGAT GGGTGGTGGC CTTCTTCAGG CAGTTCTTCA
2251 CGTCGGTGAC CAAGGTGGAC TACCTGACCT TCGGCAGGG CTTTCATCAAC
2301 GCGCATCTCT CGCAGGGCAA CAGGTTGAC TTCCACAAGT ACATCAAGAG
2351 GTCGTTGGAG GACGACTTCA AAGTCGTCGT CCGCATCAGG TACGCGCCAT
2401 TCCTTTCTCT GCACAAATTA ATACATCCAC CACCACATAG GTAGATAGAT
2451 AGATCGATAG ATAGATTATA CAAGTGCCGG TACGTACGTA CGTCTCATAT
2501 GATCTTGACA CATCTGTCCT CTTGCCGACG TCTCAAGCTC TGGTTCGTGG
2551 CGGTCCTCAT CCTCTTCCTT GATTTGACG GTAGCCGCCT TGTCCATGCC
2601 CTGCTCGCCC TCTCCTCCGC TTCTCTCCAT AATTTGTGAA CTTGTCCCGT
2651 ATATAACCAC ACCACCGTCG TCTTCTCGCA GGGATCGGCA CTCTTCTCTG
2701 GATGTCCGTG GTTCCTCTCG TGGTAAGTCC ACAATTTGAA TAGACAACCT
2751 GTCCAATTGT GATGTACAGT ACCTCCAAAC TTAATTAACA TGTCAATTGC
2801 TGATGTCTTG CGTGTAACAT TAGATCCTCT TGTGGGTGG GACCAAGCTG
2851 GAGATGGTGA TCATGGAGAT GGCCAGGAG ATCCATGACC GGGAGAGCGT
2901 CGTCAAGGGT GCTCCCGCCG TCGAGCCAG CAACAAGTAC TTCTGGTTCA
2951 ACCGGCCTGA CTGGGTCCTC TTCCTCATGC ACCTCACACT CTTCCAGAAC
3001 GCGTTTCAGA TGGCTCATTT CGTGTGGACA GTGGTACGTA CAAGTACTTG



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Figure 9C

3051 TCACTTCACT TAGGCTAACT CCAACAAACG ACCCCAAATT AATGGTCCGT
3101 CGCGTCTGTT TGGGGTATGT TTGGGGTAAA CGGACACAAA ACTCAATCCA
3151 ACGCGCGGTA GCAAACGAAC GTTTTTCCGT ACGTTTTTCGT CCGCTTTCGC
3201 CCCATCCCAG CCCAAATTCG TTGACGTTGT TGCATCGCAG GCCACGCCCCG
3251 GCTTGAAGAA ATGCTACCAC GAGAAAATGG CAATGAGCAT CGCCAAGGTC
3301 GTGCTGGGGG TAGCCGCCCA GATCTTGTGC AGCTACATCA CCTTCCCGCT
3351 CTACGCGCTC GTCACGCAGA TGGGCTCACA CATGAAGAGA AGCATCTTCG
3401 ACGAGCAGAC GGCCAAGGCG CTGACCAACT GGCGAAAGAT GGCCAAGGAG
3451 AAGAAGAAGG CCCGAGACGC GGCCATGCTG ATGGCGCAGA TGGGCGGCGG
3501 CGCGACGCCG AGCGTCGGCT CGTCGCCGGT GCACCTGCTC CACAAGGCCG
3551 GGGCGCGGTC CGACGACCCC CAGAGCGTGC CGGCGTCCCC GAGGGCCGAG
3601 AAGGAAGGCG GCGGCGTGCA GCATCCGGCG CGCAAGGTAC CTCCTTGTGA
3651 CGGGTGGAGG TCGGCCTCGT CGCCGGCGCT CGACGCTCAC ATCCCCGGTG
3701 CAGATTTTGG CTTCAGCACG CAACGTTGAC CGATCAGACA AGTTCCTTTT
3751 TTTTTCGGTG AATAGAAGCG TATCATTTCA TTGATAGACA GTAGAAATTA
3801 CAGGAATGGC TGTCTACTA CTATGTACAC AAGGGCACAG CAAAGGATCA
3851 TTGATCTTGT TACAAGAGCA GTAGAAAGGG ATTGCTCTCC ATTGATCTTG
3901 TTAAGTTGTA TGTCACAAAT TGTTGCAGAA AAAAGTGTAT GTCATCCCAA
3951 CCAAGAGCTG AGTTTGTGAT GATTCGTGCA ATAAGAATTG CAAGTTTCAC
4001 CGAGTCAAAA ATGAAGCTTC TAAGTACGCA CCAACCAACG GACTCTTTCA
4051 TCTCAACAAA AGAACTGTAA ATGGCAATAA TTCTGATAAC ATCGGAAGGG
4101 AGCTC



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Figure 10

1 ATGGCAGGTG GGAGATCGGG ATCGCGGGAG TTGCCGGAGA CGCCGACGTG
51 GGCGGTGGCC GTCGTCTGCG CCGTCCTCGT GCTCGTCTCC GCCGCCATGG
101 AGCACGGCCT CCACAACCTC AGCCATAAAA CCACCGCAGA AGTTCTCATA
151 TTTCTTGTCC TATCTGCACT TGCAGAGCTG ATGCTGCTGG GCTTCATATC
201 CCTGCTTCTC ACCGTGGCAC AGGCGCCCAT CTCCAAGATC TGCATCCCCA
251 AGTCGGCTGC CAACATCTTG TTGCCGTGCA AGGCAGGCCA AGATGCCATC
301 GAAGAAGAAG CAGCAAGTGG TCGCCGGTCC TTGGCCGGCG CCGGCGGCGG
351 GGACTACTGC TCGAAATTCG ATGGCAAGGT GCGCTGATG TCGGCAAAGA
401 GCATGCACCA GCTGCACATT TTCATCTTCG TGCTCGCCGT GTTCCATGTT
451 ACCTACTGCA TCATCACCAT GGGTTTAGGG CGCCTCAAAA TGAAGAAATG
501 GAAGAAGTGG GAGTCACAGA CCAACTCATT GGAGTATCAG TTCGCAATCG
551 ATCCTTCACG ATTCAGGTTC ACGCATCAGA CGTCGTTCGT GAAGCGGCAT
601 CTGGGATCAT TCTCAAGCAC CCCTGGGCTC AGATGGATCG TAGCATTCTT
651 CAGGCAGTTC TTTGGGTCCG TCACCAAGGT GGACTACCTG ACCATGCGGC
701 AAGGCTTCAT CAATGCGCAT TTGTCGCAGA ATAGCAAGTT CGACTTCCAC
751 AAATACATCA AGAGGTCTTT GGAGGACGAC TTCAAAGTTG TCGTTGGCAT
801 CAGCCTCCCT CTGTGGTTCG TCGGAATCCT TGTACTCTTC CTCGATATCC
851 ACGGTCTTGG CACACTTATT TGGATCTCTT TTGTTCTCTT CATCATCGTC
901 TTGTTAGTTG GGACCAAGCT AGAGATGGTG ATCATGGAGA TGGCCCAAGA
951 GATACAGGAC AGGGCCACTG TGATCCAGGG AGCACCTATG GTTGAACCAA
1001 GCAACAAGTA CTTCTGGTTC AACCGCCCTG ACTGGGTCTT GTTCTTCATA
1051 CACCTGACAC TCTTCCATAA CGCATTTTCA ATGGCGCATT TCGTATGGAC
1101 TATGGCAACA CCTGGTCTGA AGAAATGCTT CCATGAAAAT ATTTGGCTGA
1151 GCATCGTGGA AGTCATTGTG GGGATCTCTC TTCAGGTGCT ATGCAGCTAC
1201 ATCACCTTCC CGCTCTACGC GCTCGTCACA CAGATGGGAT CGAACATGAA
1251 GAAGACAATT TTCGAGGAGC AAACGATGAA GCGCTGATG AACTGGAGGA
1301 AGAAGGCGAT GGAGAAGAAG AAGGTCCGGG ACGCCGACGC GTTCCTGGCG
1351 CAGATGAGCG TCGACTTCGC GACGCCGGCG TCGAGCCGGT CCGCGTCGCC
1401 GGTGCACCTG CTGCAGGTCA CAGGGCGGGT CGGACGCCCCG CCGAGCCCAA
1451 TCACGGTGGC CTCACCACCG GCACCGGAGG AGGACATGTA CCCGGTGCCG
1501 GCGGCGGCTG CGTCTCGCCA GCTGCTAGAC GACCCGCCGG ACAGGAGGTG
1551 GATGGCATCC TCGTCGGCCG ACATCGCCGA TTCTGATTTT TCCTTCAGCG
1601 CACAACGGTG A



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Figure 11

1 ATGGCTGGGC CGGCGGGAGG TCGGGAGCTG TCGGACACGC CGACGTGGGC
51 GGTGGCGGTA GTCTGCGCCG TCATGATACT CGTCTCCGTC GCCATGGAGC
101 ACGCGCTCCA CAAGCTCGGC CACTGGTTCC ACAAGTGGCG CAAGAAGGCC
151 CTGGGGGAGG CGCTGGAGAA GATGAAGGCG GAGCTCATGC TGGTGGGCTT
201 CATATCCCTG CTCCTCATCG TCACGCAGGA TCCCGTCTCC AGGATCTGCA
251 TCTCCAAGGA GGCCGGCGAG AAGATGCTCC CGTGCAAGCC TTACGACGGC
301 GCCGGCGGTG GCAAAGGCAA GGACAATCAC CGGAGGCTTC TCTGGCTCCA
351 AGGCGAGAGC GAGACCCACC GCCGGTTCCT GGCTGCCCCG GCCGGAGTGG
401 ACGTCTGCGC CAAACAGGGC AAGGTGGCGC TGATGTCAGC GGAAGCATG
451 CACCAACTGC ACATATTCAT CTCGTGCTC GCCGTCTTCC ACGTCTTGTA
501 CAGCGTCGTC ACCATGACCC TAAGCCGTCT CAAAATGAAG CAATGGAAGA
551 AGTGGGAGTC GGAGACCGCC TCGCTGGAGT ATCAGTTCGC GAATGATCCA
601 TCGCGGTGCC GGTTCACGCA CCAGACGACG TTGGTGAGGC GGCACCTGGG
651 CCTCTCCAGC ACCCCCGGCG TCAGATGGGT GGTGGCCTTC TTCAGGCAGT
701 TCTTCACGTC GGTGACCAAG GTGGACTACC TGACCTTGCG GCAGGGCTTC
751 ATCAACGCGC ATCTCTCGCA GGGCAACAGG TTCGACTTCC ACAAGTACAT
801 CAAGAGGTCG TTGGAGGACG ACTTCAAAGT CGTCGTCCGC ATCAGTCTCA
851 AGCTCTGGTT CGTGGCGGTC CTCATCCTCT TCCTTGATTT CGACGGGATC
901 GGCACTCTTC TCTGGATGTC CGTGGTTCCT CTCGTGATCC TCTTGTGGGT
951 TGGGACCAAG CTGGAGATGG TGATCATGGA GATGGCCCAG GAGATCCATG
1001 ACCGGGAGAG CGTCGTCAAG GGTGCTCCCG CCGTCGAGCC CAGCAACAAG
1051 TACTTCTGGT TCAACCGGCC TGA CTGGGTC CTCTTCCTCA TGCACCTCAC
1101 ACTCTTCCAG AACGCGTTTC AGATGGCTCA TTTCGTGTGG ACAGTGGCCA
1151 CGCCCGGCTT GAAGAAATGC TACCACGAGA AAATGGCAAT GAGCATCGCC
1201 AAGGTCGTGC TGGGGGTAGC CGCCAGATC TTGTGCAGCT ACATCACCTT
1251 CCCGCTCTAC GCGCTCGTCA CGCAGATGGG CTCACACATG AAGAGAAGCA
1301 TCTTCGACGA GCAGACGGCC AAGGCGCTGA CCAACTGGCG AAAGATGGCC
1351 AAGGAGAAGA AGAAGGCCCG AGACGCGGCC ATGCTGATGG CGCAGATGGG
1401 CGGCGGCGCG ACGCCGAGCG TCGGCTCGTC GCCGGTGCAC CTGCTCCACA
1451 AGGCCGGGGC GCGGTCCGAC GACCCCCAGA GCGTGCCGGC GTCCCCGAGG
1501 GCCGAGAAGG AAGGCGGCGG CGTGCAGCAT CCGGCGCGCA AGGTACCTCC
1551 TTGTGACGGG TGGAGGTCGG CCTCGTCGCC GCGCTCGAC GCTCACATCC
1601 CCGGTGCAGA TTTTGGCTTC AGCACGCAAC GTGA



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Figure 12A

1 GTTGGTACAT AAAAGACTCT TCCTTTGTCT GTTTTTTGTT CCCAGATTCA
51 TCTTTACTTA TTGACTAAAT TCTCTCTGGT GTGAGAAGTA AAATGGGTCA
101 CGGAGGAGAA GGGATGTCGC TTGAATTCAC TCCGACGTGG GTCGTCGCCG
151 GAGTTTGTAC GGTCATCGTC GCGATTCAC TGGCGGTGGA GCGTTTGCTT
201 CACTATTTTCG GTACTGTTCT TAAGAAGAAG AAGCAAAAAC CCCTTTACGA
251 AGCCCTTCAA AAGGTTAAAG AAGAGCTGAT GTTGTTAGGG TTTATATCGC
301 TGTTACTGAC GGTATTCCAA GGGCTCATTT CCAAATTCTG TGTGAAAGAA
351 AATGTGCTTA TGCATATGCT TCCATGTTCT CTCGATTCAA GACGAGAAGC
401 TGGGGCAAGT GAACATAAAA ACGTTACAGC AAAAGAACAT TTTCAGACTT
451 TTTTACCTAT TGTTGGAACC ACTAGGCGTC TACTTGCTGA ACATGCTGCT
501 GTGCAAGTTG GTTACTGTAG CGAAAAGGGT AAAGTACCAT TGCTTTCGCT
551 TGAGGCATTG CACCATCTAC ATATTTTCAT CTTCGTCCTC GCCATATCCC
601 ATGTGACATT CTGTGTCCTT ACCGTGATTT TTGGAAGCAC AAGGATTCAC
651 CAATGGAAGA AATGGGAGGA TTCGATCGCA GATGAGAAGT TTGACCCCGA
701 AACAGCTCTC AGGAAAAGAA GGGTCACTCA TGTACACAAC CATGCTTTTA
751 TTAAAGAGCA TTTTCTTGGT ATTGGCAAAG ATTCAGTCAT CCTCGGATGG
801 ACGCAATCCT TTCTCAAGCA ATTCTATGAT TCTGTGACGA AATCAGATTA
851 CGTGACTTTA CGTCTTGGTT TCATTATGAC ACATTGTAAG GGAAACCCCA
901 AGCTTAATTT CCACAAGTAT ATGATGCGCG CTCTAGAGGA TGATTTCAAA
951 CAAGTTGTTG GTATTAGTTG GTATCTTTGG ATCTTTGTCG TCATCTTTTT
1001 GCTGCTAAAT GTTAACGGAT GGCACACATA TTTCTGGATA GCATTTATTC
1051 CCTTTGCTTT GCTTCTTGCT GTGGGAACAA AGTTGGAGCA TGTGATTGCA
1101 CAGTTAGCTC ATGAAGTTGC AGAGAAACAT GTAGCCATTG AAGGAGACTT
1151 AGTGGTGAAA CCCTCAGATG AGCATTTCTG GTTCAGCAAA CCTCAAATTG
1201 TTCTCTACTT GATCCATTTT ATCCTCTTCC AGAATGCTTT TGAGATTGCG



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Figure 12B

1251 TTTTCTTTT GGATTGGGT TACATACGGC TTCGACTCGT GCATTATGGG
1301 ACAGGTGAGA TACATTGTTC CAAGATTGGT TATCGGGGTC TTCATTCAAG
1351 TGCTTTGCAG TTACAGTACA CTGCCTCTTT ACGCCATCGT CTCACAGATG
1401 GGAAGTAGCT TCAAGAAAGC TATATTCGAG GAGAATGTGC AGGTTGGTCT
1451 TGTTGGTTGG GCACAGAAAG TGAAACAAAA GAGAGACCTA AAAGCTGCAG
1501 CTAGTAATGG AGACGAAGGA AGCTCTCAGG CTGGTCCTGG TCCTGATTCT
1551 GGTTCTGGTT CTGCTCCTGC TGCTGGTCCT GGTGCAGGTT TTGCAGGAAT
1601 TCAGCTCAGC AGAGTAACAA GAAACAACGC AGGGGACACA AACAAATGAGA
1651 TTACACCTGA TCATAACAAC TGAGCAGAGA TATTATCTTT TCCATTTAGA
1701 GGATCATCAT CAGATTTTAG CTTCAAGGTC CGGTTTTGTG GTTTATACAT
1751 AAGTTATAGT GACTTGATTT TTTTGTTTTG TTACAAAGTT ACCATCTTTG
1801 GATTAGAATT GGGAAATTGA ATCTGTTTGT ATATTGTATT ATTTGGAACA
1851 TTGTGGATGC CCATGGATAT GTTTCTGTTC



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Figure 13

1 MAGGRSGSRE LPETPTWAVA VVCAVLVLVS AAMEHGLHNL SHKTTAEVLI
51 FLVLSALAE LMLGFISLLL TVAQAPISKI CIPKSAANIL LPCKAGQDAI
101 EEEAASGRRS LAGAGGGDYC SKFDGKVALM SAKSMHQLHI FIFVLAVFHV
151 TYCIITMGLG RLKMKKKKKW ESQTNSELYQ FAIDPSRFRF THQTSFVKRH
201 LGSFSSTPGL RWIVAFFRQF FGSVTKVDYL TMRQGFINAH LSQNSKFDFH
251 KYIKRSLEDD FKVVGISLP LWFVGILVLF LDIHGLGTLI WISFVPLIIV
301 LLVGTKLEMV IMEMAQEIQD RATVIQGAPM VEPSNKYFWF NRPDWVLEFI
351 HLTLFHNAFQ MAHFVWTMAT PGLKKCFHEN IWLSEIVEVIV GISLQVLCSY
401 ITFPLYALVT QMGSNMKKTI FEEQTMKALM NWRKKAMEKK KVRDADAFLA
451 QMSVDFATPA SSRSASPVHL LQVTGRVGRP PSPITVASPP APEEDMYPVP
501 AAAASRQLLD DPPDRRWAS SSADIADSDF SFSAQR*



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Figure 14

1 MAGPAGGREL SDTPTWAVAV VCAVMILVSV AMEHALHKLG HWFHKWRKKA
51 LGEALEKMKA ELMLVGFISL LLIVTQDPVS RICISKEAGE KMLPCKPYDG
101 AGGGKKGKDNH RRLWLQGES ETHRRFLAAP AGVDVCAKQG KVALMSAGSM
151 HQLHIFIFVL AVFHVLYSVV TMTLSRLKMK QWKKWESETA SLEYQFANDP
201 SRCRFTHQTT LVRRHLGLSS TPGVRWVAV FRQFFTSVTK VDYLTLRQGF
251 INAHLSQGNR FDFHKYIKRS LEDDFKVVR ISLKLWVAV LILFLDFDGI
301 GTLLWMSVVP LVILLWVGTK LEMVIMEMAQ EIHDRESVVK GAPAVEPSNK
351 YFWFNRPDWV LFLMHLTLFQ NAFQMAHFVW TVATPGLKKC YHEKMAMSIA
401 KVVLGVAQI LCSYITFPLY ALVTQMGSIM KRSIFDEQTA KALTNRKMA
451 KEKKKARDAA MLMAQMGGGA TPSVGSSPVH LLHKAGARSD DPQSVPASPR
501 AEKEGGGVQH PARKVPPCDG WRSASSPALD AHIPGADFGF STQR*



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Figure 15

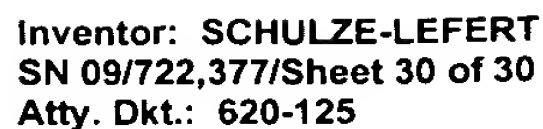
1 MGHGGEGLMSL EFTPTWVVAG VCTVIVAISL AVERLLHYFG TVLKKKKQKP
51 LYEALQKVKE ELMLLGFISL LLTVFQGLIS KFCVKENVLM HMLPCSLDSR
101 REAGASEHKN VTAKEHFQTF LPIVGTTRRL LAEHAAVQVG YCSEKGVPL
151 LSLEALHHLH IFIFVLAISH VTFCVLTIVF GSTRIHQWKK WEDSIADKFK
201 DPETALRKRR VTHVHNHAFI KEHFLGIGKD SVILGWTQSF LKQFYDSVTK
251 SDYVTLRLGF IMTHCKGNPK LNFHKYMMRA LEDDFKQVVG ISWYLVWIFVV
301 IFLLLVNNGW HTYFWIAFIP FALLLAVGTK LEHVIAQLAH EVAEKHVAIE
351 GDLVVKPSDE HFWFSKPQIV LYLIHFILFQ NAFEIAFFFW IWVTYGFDSK
401 IMGQVRYIVP RLVIGVFIQV LCSYSTLPLY AIVSQMGSSF KKAIFEENVQ
451 VGLVGWAQKV KQKRDLCAAA SNGDEGSSQA GPGPDGSGGS APAAGPGAGF
501 AGIQLSRVTR NNAGDTNNEI TPDHNN*



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Figure 16A

Hvml0-H1 Mlo Osmlo-H1m Atmlo-H1 Consensus	MAGPAG MSDCKKGV MAGGRS MGHGGEGM M	GR V S G G	ELSD ELPE ELPE SLEF EL	TPTWAV TPTWAV TPTWAV TPTWAV TPTWAV	AVVCAVM AVVFAAM AVVCAV AGVCTVI AVVCAV	ILV VLV VLV VAV VLV	SVAMEH SVLMEH SAAMEH SLAVER S	ALHK GLHK GLHN LLHY LH	LGHWF LGHWF LSH FGTV LGH	WK HRHK KTA KKKQ K	KALGEAL KALWEAL EVLIFLV KPLYEAL KLEAL	MEK M LSA QK K
Hvml0-H1 Mlo Osmlo-H1m Atmlo-H1 Consensus	KAELML KAELML LAELML KEELML KAELML	VGF VGF LGF LGF GFI	SLLL SLLL SLLL SLLL SLLL	ITQDPP ITQDPP ITQDPP ITQDPP ITQDPP	VSRICISKE IAKICISED ISKICIPKS LSKFCVKEN ISKICI	SK SED PKS KEN --	AGKMLP AADVMW AANILP VLMHML A	PC PC PC PC PC	KPYDGA K KAGQDA KREAGASE K	GG IE SE -- A	GKGDNDHRRRL RGTEGRKPS EEAASGRRS HKNVTAKKEHF --	
Hvml0-H1 Mlo Osmlo-H1m Atmlo-H1 Consensus	LWLQGESETH KYVD QTFLP QTFLP QTFLP	AGV AGV AGV AGV AGV	RRFLA RRFLA RRFLA RRFLA RRFLA	LAAGGG LAAGGG LAAGGG LAAGGG LAAGGG	DVCAKQ YCP CSKFDGK QVGYCSEK --	QK EGK EGK EGK EGK	VALMS VALMS VALMS VALMS VALMS	AGSMH AGSMH AGSMH AGSMH AGSMH	QLHIFIFVLA QLHIFIFVLA QLHIFIFVLA QLHIFIFVLA QLHIFIFVLA	LA LA LA LA LA	VFHVLYSVV VFHVLYSVV VFHVLYSVV VFHVLYSVV VFHVLYSVV	
Hvml0-H1 Mlo Osmlo-H1m Atmlo-H1 Consensus	MTLSRL IALSRL MGLSRL VIFGS --	RLK RLK RLK RLK RLK	WKKWE WKKWE WKKWE WKKWE WKKWE	SETAS SETAS SETAS SETAS SETAS	LEYQFANDPS LEYQFANDPS LEYQFANDPS LEYQFANDPS LEYQFANDPS	DP DP DP DP DP	RCRFT RCRFT RCRFT RCRFT RCRFT	HQT HQT HQT HQT HQT	TVRRHLG TVRRHLG TVRRHLG TVRRHLG TVRRHLG	LG LG LG LG LG	SSSTPGV SSSTPGV SSSTPGV SSSTPGV SSSTPGV	
Hvml0-H1 Mlo Osmlo-H1m Atmlo-H1 Consensus	VAFFRQ VAFFRQ VAFFRQ VAFFRQ VAFFRQ	FFTS FFTS FFTS FFTS FFTS	VTKVDD VTKVDD VTKVDD VTKVDD VTKVDD	YLTTLR YLTTLR YLTTLR YLTTLR YLTTLR	QGFINA QGFINA QGFINA QGFINA QGFINA	HL HL HL HL HL	GNRFFD GNRFFD GNRFFD GNRFFD GNRFFD	FHKYI FHKYI FHKYI FHKYI FHKYI	KRSL KRSL KRSL KRSL KRSL	EDDFKV EDDFKV EDDFKV EDDFKV EDDFKV	FW FW FW FW FW	
Hvml0-H1 Mlo Osmlo-H1m Atmlo-H1 Consensus	VAVLIL VAILL VAILL VAILL VAILL	FLDF FLDF FLDF FLDF FLDF	DGIGT DGVGT DGVGT DGVGT DGVGT	LLWMS LLWMS LLWMS LLWMS LLWMS	VVPLV VVPLV VVPLV VVPLV VVPLV	LLV LLV LLV LLV LLV	GTKLEM GTKLEM GTKLEM GTKLEM GTKLEM	VIME VIME VIME VIME VIME	MAQEI MAQEI MAQEI MAQEI MAQEI	HDRAS HDRAS HDRAS HDRAS HDRAS	VEP VEP VEP VEP VEP	
Hvml0-H1 Mlo Osmlo-H1m Atmlo-H1 Consensus	SNKYFW SNKYFW SNKYFW SNKYFW SNKYFW	NRPP NRPP NRPP NRPP NRPP	DWVLF DWVLF DWVLF DWVLF DWVLF	LMHLLT LMHLLT LMHLLT LMHLLT LMHLLT	LFQNA LFQNA LFQNA LFQNA LFQNA	MAH MAH MAH MAH MAH	FVWT FVWT FVWT FVWT FVWT	ATPGL ATPGL ATPGL ATPGL ATPGL	KKCYH KKCYH KKCYH KKCYH KKCYH	EKMAM EKMAM EKMAM EKMAM EKMAM	GLA GLA GLA GLA GLA	

[illegible]